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RAW SEQUENCE LISTING

SATE: 6218/27/1 TIME: 18:8c:85

PATENT APPLICATION: US/09/851,410

Input Set : N:\Crf3\RULE60\09851410.txt Output Set: N:\CRF3\06152001\1851410.raw

SEQUENCE LISTING

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ENTERED
      3 (1) GENERAL INFORMATION:
             (1) APPLICANT: Reyes, Gregory R
                              Yarbough, Patrice U
                             Bradley, Daniel W
      8
                             Hráwczynski, Krzysztól 2
                              Tam, Albert
     10
                             Fry, Kirk E
     1.
            (ii) TITLE OF INVENTION: DNA Dequences of Enteridally Transmitted
     1.3
                                       Non-A/Non-B Hepatitis Viral Agent
           (iii) NUMBER OF SEQUENCES: 20
     14,
     1...
            (iv) CORRESPONDENCE ADDRESS:
     18
                   ·A) ADDRESSEE: Dehlinger & Associates
     1.9
                    B) STREET: 350 Cambridge Avenue, Suite 250
     20
                    C) CITY: Palc Alto
     .11
                    E) STATE: CA
                    E) COUNTRY: USA
                   ·F) ZIE: 94306
     : \mathcal{G}
             (v) COMPUTER READABLE FORM:
                   (A) MEDIUM TYPE: Floppy disk
                   (F) COMPUTER: IBM PC compatible
                   (C) OPERATING SYSTEM: FC-DOS/MS-DOS
     _1 E
     39
                   (D) SOFTWARE: PatentIr Release #1.0, Version #1.25
            (vi) CUERENT APPLICATION DATA:
     \sim 1
C--> 32
                   (A) APPLICATION NUMBER: US/09/851,410
C--> 33
                   (B) FILING DATE: 07-May-2001
     1, ⊊
           (vii) PEIOR APPLICATION DATA:
                   (A) APPLICATION NUMBER: 09/128,275
     n Kr
     37
                   (B) FILING DATE:
     40
                   (A) APPLICATION NUMBER: US 07/681,078
                   (B) FILING DATE: CD-AFR-1991
     41
                   (A) APPLICATION NUMBER: US COLUNG, 888
     44
     4.0
                   B) FILING DATE: (3-AFR-1944
                   -A) APPLICATION NUMBER: US 17 42.,921
     3 8
     49
                   B) FILING DATE: 13-OCT-1989
                   A) APPLICATION NUMBER: US 07 367,486
                   b) Filing DATE: 16-JUN-1989
     19.7
                   (A) APPLICATION NUMBER: US CO 530, eC2
     1) (1
                    B) FILING DATE: 11-AFR-1983
                   (A) APPLICATION NUMBER: US 11.18, 447
     ń(
                   .B. FILING DATÉ: IN-JUN-1984
     \circ 1
          (viii) ATTORNEY AGENT INFORMATION:
     65
     194
                   (A. NAME: Fetithery, Coanne B.
                   (P) REGISTRATION NUMBER: 41, 42
     6.5
                    TO ROPERENCE POURET NUMBER: 4.
                                                     - 1 - 3 . . . . .
     ΰť
             (ix) TELEPRIMUDICATION INFORMATION:
     p \in \mathbb{R}
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AT TELEFRONE: 166 1 304- 6-





RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/851,410

TATE: Woll 1 1

Input Set : N:\Crf3\RULE60\09851410.txt
Output Set: N:\CRF3\06152001\1851410.raw

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            (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 1295 base pairs
     76
                   (B, TYPE: nucleic acid
     -- 3
                   (C) STRANDEDNESS: double
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                  (D) TOFOLOGY: linear
W--> 80
            (ii) MOLECULE TYPE: DNA
           (iii) HYP THETICAL: NO
     8.3
     8.1
           (iv) ANTI-SENSE: NO
     86
            (vi) DRIGINAL SOURCE:
     ٠ ع
                  (C) INDIVIDUAL ISOLATE: 1.35 kb EdeRI insert of ET1.1,
     ž. ...
                                           forward sequence
     4 1
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     91
                  (A) NAME/HEY: CDS
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                  (B) LOCATION: 1..1293
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     9 +
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                   (B) LOCATION: 3..1295
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             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     10.3
     1) & AGADOTISTOC CTGTTGCAGO PGTTCTACCA CCCTGCCCCG AGCTCGAACA GGGCCTTCTC
                                                                                  60
     10.7 TAGCTSCCCC AGGAGCTCAC CACCIGIGAT AGTGTCGTAA CATTIGAATT AACAGACATT
                                                                                 120
     109 STGCASTGCC GCATGGCCGC CCCGAGCCAG CGCAAGGCCG TGCTGTCCAC ACTCGTGGGC
                                                                                 180
     111 OGCTACGGGG GTOGGGACAAA GCTCTACAAT GCTTCCCCACT CTGATGTTCG CGACTCTCTC
                                                                                 240
     115 GOOCSTTTTA TOCOGGOCAT TGGOCCOGTA CAGGTTACAA CTTGTGAATT GTACGAGCTA
                                                                                 311
     1.5 GTGGAGGCCA TGGTCGAGAA GGGCCAGGAT GGCTCCGGGG TCCTTGAGCT TGATCTTTGC
                                                                                 Bril.
     117 AAGGETSAGG TSTCCASGAT CACCITITE CAGAAAGATT GTAACAAGTT CACCACAGGT
                                                                                 420
     119 SAGACCATTG COCATGSTAA AGT3G3CCAG GSCATCTCGG CCTGGAGCAA GACCTTCTGC
                                                                                 4 € C
     1.1 GCCCTCTTG GCCCTTGGIT CCGCGCTATT GAGAAGGCTA TTCTGGCCCT GCTCCCTCAG
                                                                                 5,40
                                                                                 600
     113 GETETETTT ACCEPSATEC CTTPGARGAC ACCETCTTCT COECGGCRET GGCCGCASCA
     115 AAGGCATCCA TGGTGTTTGA GAATGACTTI TCTGAGTTTG ACTCCACCCA GAATAACTTT
                                                                                 6 til
     107 TOTOTGBETO TABAGTGTEC TATTATEGAS GAGTGTGGGA TGCCGCAGTG GCTCATCCGC
                                                                                 720
     1:9 CTGTATCACC TTATAAGGIC IGCGTGGATC TTGCAGGGCC CGAAGGAGTC TCTGCGAGGG
                                                                                 780
     1:1 FTTTGGAAGA AACACTCC3G TGA3CC3GGC ACTCTTCTAT GGAATACTGT CIGGAATATG
                                                                                 840
     183 GOOGTTATTA COCACTETTA TGASTFEEGG GATTTTCAGG TGGCTGCCTT TAAAGGTGAT
                                                                                 900
                                                                                 900
     155 GATTOGATAG TGCTTTGCAG FGAGTATCGT CAGACTCCAG GAGCTGCTGT CCTGATCGCC
     1:7 GOODGTGGOT TGAAGTTGAA GGTAGATITC CGCCCGATOG GTTTGTATGC AGGTGTTGTG
                                                                                1000
     149 BIGGOCODOS GOCTIGACAS GOTOCOTRAT GITOTGOGOT TOGOCOGGOOG GOTTACOGAS
                                                                                1050
     141 AAGAATTEEG GOCCIGECIC TONECEEGCE GAGCAGOTON GOCTOEGTET TAGTGATTTC
                                                                                1145
     143 DICCOCCAGAGO TOACCAATST ACCTCAGATG TOTSTERATU TISTITOCCG IGTITATGGG
                                                                                1200
     145 STTTOCOOTS GACTOSTICA TAACOIGATI GGCATSCIAN AGGCTGTIGO TPATGGCAAG
                                                                                1260
     14% GCACATTICA CIGAGICAGI AAAACGAGIG CICGA
                                                                                1295
     150 (2) INFORMATION FOR SEQ ID NO: 2:
              (1) SEQUENCE CHARACTERISTICS:
     152
                   ,A, :ENGTH: 431 Amino arido
     153
     1 5 4
                   (F TYPE: amino acid
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/851,410

Input Set : N:\Crf3\RULE60\09851410.txt
Gutput Set: N:\CRF3\06152001\1851410.raw

Tofology: timear (ii) MOLECULE TYFE: protein (xi) SEPTENTE DESCRIPTION: GEQ II II : A: 16] Arg Pro Val Bro Val Ala Ala Val Let Bro Bro Typ Bro Blt Let Blt 16.1 1 164 Glm Gly Leu Leu Tyr Leu Fri Glm Glu Leu Thr The Tye Asp Yer Val 16 Val Thr Phe Glu Leu Thr Asp Ile Val His Tys Arg Met Ala Ala Fro 16: 170 Ser 3ln Arg Lys Ala Val Leu Ser Thr Leu Val Gly Arg Tyr Gly Gly 171 50 175 Arg Thr Lys Leu Tyr Ash Ala Ser His Ser Asp Mal Arg Asp Ser Leu 20 174 65 176 Ala Arq Phé lle Fro Ala Ile Gly Fro Val Glm Val Thr Thr Cys Glu ×5 17g Leu Tyr Glu Leu Val Glu Ala Met Val Glu Lys Gly Gln Asp Gly Ser 105 100 19. Ala Vai Leu Glu Leu Asp Leu Cys Ash Arg Asp Wal Ser Arg Ile Thr 115 120 186 Pne Pho Glr. Lys Asp Cys Asn Lys Fhe Thr Thr Gly Glu Thr Ile Ala 135 1.30 180 His Gly Lys Val Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr Phe Cys 189 145 150 159 191 Ala Leu Phe Gly Pro Trp Phe Arg Ala Ile Glu Lys Ala Ile Leu Ala 170 165 194 Leu Leu Pro Gln Gly Val Phe Tyr Gly Asp Ala Phe Asp Asp Thr Val 1*a*· 180 185 197 Phe Ser Ala Ala Val Ala Ala Ala Lys Ala Ser Met Val Phe Glu Asn 198 195 200 205 200 Asp Phe Ser Glu The Asp Ser Thr Gln Ash Ash The Ser Let Gly Leu 214 20 - Glu Cys Ala The Met Glu Glu Cys Gly Met Fro Un Trp Leu Iie Arg 204 225 230 20% Leu Tyr His Leu Ile Arg Ser Ala Trp Ile Leu Gln Ala Pro Lys Glu 250 200 Ser Leu Arg Gly Fhe Trp Lys Lys His Sor Gly Glu Fro Gly Thr Leu 260 265 210 21. Leu Trp Asn Thr Val Trp Asn Met Ala Val Ile Thr His Cys Tyr Asp 275 21: 280 21: Phe Arg Asp Fhe Gln Val Ala Ala Phe Lys Cly Asp Asp Ser Ile Val 0.95 21. 290 lir Leu Cys Ser Gin Tyr Arg Gin Ser Erc Sly Ala Ala Val Leu Ile Ala 21 + 305 310 221 Gly Cys Gly Led bys Lea bys Val Asp The Arr Pro Ile Bly Lea Tyr 224 Ala Gly Wal Val Mal Ala Fro Sly Leu Bly Ala Leu Fro Asp Wal Wal 22 Arg Phe Ala Sty Arg Len Thi Sty Lys Ash Try Sty Tr Sty in Sty

18

20





RAW SEQUENCE LISTING

HATENT APPLICATION: US/09/851,410

TATE: L*15 Ladi TIME: 15:50:56

Input Set : N:\Crf3\RULE60\09851410.txt Sutput Set: N:\CRF3\06152001\I851410.raw

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230 Arg Ala Glo Glo Dea Ara bea Ala Cal Cer Asg Ene bea Ara bya bea
233 Thr Ash Val Ala 31h Met Dys Mai Asp Val Val der Arg Val Tyr 31;
141 385
                       330
150 Val Ser Pro Sly Leu Val His Ash Leu II.e Sly Met Leu Sin Ala Val
                   425
ing Ala Asp Gly bys Ala His Phe Thr Glu Cer Vai bys Pro Val Leu
           420
, i.e. (2) INFORMATION FOR SEQ ID NO: \beta:
212
       i) SEQUENCE CHARACTERISTICS:
```

- A) LENGIH: 13 base pairs 246
- . 4 B) TYPE: nucleic acid
 - TRANDEDUESS: single
 - DFOLOGY: linear

(11) MOLECULE TYPE: DNA W--> 251

. 44

. . 4 भ

. 141,

2.44

- 153 (iii) HYPOTHETICAL: NO
- 185 (LV) ANTI-SENSE: NO
- 257 (vi) ORIGINAL SOURCE:
- 3) INDIVIDUAL ISCLATE: linker top (5') sequence ..53
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: 1511
- . HE GGAATTCGCS SIGGSTCS
- 105 (2) INFORMATION FOR SEQ ID NO: 4:
- 267 (1) SEQUENCE CHARACTERISTICS:
- $t_0 =$ A) LENGTH: 2) base pairs
- $-i_1 +$ HET TYPE: nucleic acid
 - IT STRANDELMESS: single
- -D- TOPOLOGY: linear

(11) MOLECULE TYPE: DNA W--> 273

- 200 (iii) HYPOTHETICAL: NO
- (:v) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (3) INDIVIDUAL ISCLATE: linker bottom (3) sequence .. 80
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: .182
- L84 CGAGOGGCCG GSAATTCCTT
- L86 (2) INFORMATION FOR SEC ID NO: 5:
- ..F3 (1) SEQUENCE CHARACTERISTICS:
- . }- -4 A: LENGTH: 1295 base pairs
 - B) TYPE: nurleic acid
- C) STRANDEINESS: double . 41 . . .
 - D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA W--> 294

- (iii) HYPOTHETICAL: NO
- . '4" (.v) ANTI-SENSE: NO
- ×(00° ("i) ORIGINAL SOURCE:
- -01 (C) INDIVIDUAL ISOLATE: 1.33 kb Ecoki insert of ETI.1,
- reverse sequence
- (Mi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
- HOT TOGAGOACTS STITTAGTON CTONGTONNA TOTALITY TOTAL NATURALISAN AGARTGENES 60
- SCO ATGCCAATCA CATTATOMAC CASTITTADA CATATOMA CATATOMA AMAGAA AGAA AMAGAACATOM





DATE: 10/15 1 1

TIME: 15: 0:14

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/851,410

Input Set : N:\Crf3\RULE60\09851410.txt Sutput Set: N:\CRF3\06152001\1851410.raw

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311 ACADADATOT CAGOTACATT OGTCAGOTTG OGGAGGAAAT CAGTAACAGO GAGGGGGAGC	180
311 ACADACATOT CAGOTACATT OGTGAGOTTG OGGAGGAAL CAGTAACAGO MIDDISARGATO 312 TG:TTOGTOC COTCAGGGC AGGGCUCCAA MIDITOTOGG TAAGGCGGCC UUDISARGATO 312 TG:TTOGTOC COTCAGGGCC AGGGCGCAGAALA CAGGCGATA CAAACCGATO	140
312 TG:TTOGTOC COTOAGGGOO AGGGOOCCAA TESTEE OLOCTOCATA CAAACCGATC	3.30
31 ACHANAT AG CCAGGGGGC AAGACCAGGA GCGGGGGG TGGGGAAGA LGCTGGTGGA	360
31 ACHANAT NAG GCAGCGCGCC AAGGCCGGGG GCCACCACAA GTCACGACAGC AGCTGCTGGA 31 GGGC FGARAT CTACCTTCAA CTTCAAGCCA CAGCCGGCGA CCCTGAAAGGC AGCCACCTGA	429
	430
31 / CTITHADRAT ACTOACTGOA AAGUALT GAALTATU TOOAGAGAGT ATTOCATARA 31 AAAT 331 GA ACTOATAACA GTGUGTAATA ACGGOOATAT TOOAGAGAGT ATTOCATARA 321 AAAT 331 GA ACTOATAACA GTGUGTAATA ACGGOOATAT TOOAGAGAGTO CTTOURGGOO	540
	650
	660
31. TG:AAGATOO AAGCAGACOT TATAAGGTGA TATAAGGTGA ISTOCTOGGT GGAGTCAAAC 31 CANTINTINA IMATAGCADA CICTAGACOC AGAGAAAAGT TATTOTGGGT GGAGTCAAAC	720
31 / CANTINTINA IMATAGOADA CICTAGACCO AGAGAMAASI IAITOTSSI CGCCGAGAAG 31 / TONGAAAAGI WATTOTCAAA CADCATGOAT GCCTTTOCTO CGGCCACAGO CGCCGAGAAG	780
	840
3-1 ACGGTGTTAT TAAAGGCATC ACUGTAAAAC ACACCOTORS SERBOTOTTGCT CCAGGCCGAG 3-3 TTCTCAATAG TGCGGAACCA AUGGCCAAAG AGGGCGCAGA AGGTCTTGCT CCAGGCCGAG 3-3 TTCTCAATAG TGCGGAACCA AUGGCCAAAG AGGGCGCAGA AGGTCATACAATCT	90 J
3:3 TTCTCAATAG 'GCGCAACCA ACGGCAATC AGGGCGAACTG TGGTGAACTT GTTACAATCT 3:3 ATGCCCT3GC CCACCTTAGC ACGGCCTAGCAA GACCAAGCTC AAGGACGGCG	960
FIG ATGCCCTRGC CACCTTARC ARESE MAIG GICTORCIO IDDICAGOTO AAGGACGGCG FIRST TTCTGCAAGA AGGIGATORT GGACARGCT GOTACAATTO ACAAGTTGTA	1020
TTOTGCAAGA AGGIGATOOT GABA.GTCA GGGITGCAAA GAICATOTA ACAAGTTGTA 359 GAGCCATOOT GGCCCTTOTO GACCAGTGAA AGTCGCGAAC ATCAGAGTGG	1020
349 GAGCCATOOT BECONTICTS MANUALIGED TOOACTAGOT COINCIANTA 341 ACCTOTACEG EECCAATEGO TOOGGATAAAA CGGGCGAGAG AGTCGCGAAC ATCAGAGTGG 341 ACCTOTACEG EECCAATEGO TOOGGATAAAA CAGGGCGCCA CGAGTGTGGA CAGCACGGCC	1140
341 ACCTOTAGEG BECCHATESE GOURGEOUS TAGGGGCCCA CGAGTGTGGA CAGCAGGGCC 343 GAAGGATTGT AGAGGTTTGT GOURACGGCCCA TAGGGGCCCA CGAGTGTGAATTC AAATGTTAGG	1200
343 GAAGCATTGT AGAGCTTTGT GCGACCGCCG TAGCGGCCCA CGNGTGTTAATTC AAATGTTACG 345 TTGCGCTGGC TCGGGGGGGCCC CATGCGGCAG TGCACAATGT CTGTTAATTC AAATGTTACG	1260
A STANDARD TO THE TAIL A COMPANY THE TAIL A STANDARD A STANDARD TO COOL TO STANDARD TO COOL TO STANDARD TO COOL TO STANDARD TO STANDARD TO COOL TO COO	1295
34 ACAGGOTGUTA GAACAGOTGO AACAGGGACA GGTOT	1200
CHI ATTEMPT OF THE PROPERTY OF THE SECOND SE	
374 (1) SEQUENCE CHAFACTERISTICS:	
355 (A) LEASIN: 113, 6455 PATTS	
ner of the state o	
356 /E) TYPE: nucleic acid	
W> 367 (C) STRANDEDNESS: HEV - Burma strain	
W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOFOLOGY: linear	
W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOFOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA	
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W> 367 318 W> 360 362 319 364 364 366 (v) OFIGINAL COURCE:	
W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOPOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA (iv) AUTI-SENSE: DE (iv) AUTI-SENSE: DE (vi) OFIGINAL COUFCE: (ix) FEATUPE:	
W> 367 (C) STRANDEDNESS: HEV - Burma Strain (E) TOFOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA (iii) HYLOTHECLICAL: IX (iv) ANTI-SENSE: IX (iv) ANTI-SENSE: IX (vi) OFIGINAL COUPCE: (iii) FEATUFE: (A) NAME FEY: COS (A) NAME FEY: COS	
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W> 367 (C) STRANDEDNESS: HEV - Burma Strain (E) TOFOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA 362 (iii) HYFOTHECTICAL: IN (iv) ANTI-SENSE: IN (iv) OFIGINAL DOUBCE: (iv) FEATURE: (iv) FEATURE: (A) NAME FEY: COS (B) LOCATION: 385106 (iv) FEATURE:	
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W> 367 (C) STRANDEDNESS: HEV - Burma Strain (E) TOPOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA (iii) HYLOTHECLICAL: No (iv) AUTI-SENSE: DO (iv) OFIGINAL COURCE: (iv) FFATURE: (iv) FFATURE: (iv) FFATURE: (iv) FEATURE: (iv) HAME (MEM: CDO)	
W> 367 (C) STRANDEDNESS: HEV - Burma Strain (E) TOPOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA 362 (iii) HYLOTHETICAL: ID. 364 (iv) ANTI-SENSE: ID. 366 (vi) OFLGINAL COUPCE: 366 (ix) FEATURE: 376 (ix) FEATURE: 377 (ix) FEATURE: 378 (ix) FEATURE: 379 (ix) FEATURE: 370 (ix) FE	
W> 367 318 (C) STRANDEDNESS: HEV - Burma strain 318 (F) TOFCLOSY: linear W> 360 (ii) MOLECULE TYPE: DNA 362 364 (iv) ANTI-SENSE: DC 366 (vi) OFIGINAL COURCE: 366 (vi) OFIGINAL COURCE: 367 (iii) FEATUFE: 377 (iii) FEATUFE: 378 (iv) FEATUFE: 379 (iv) FEATUFE: 370 (iv) FEATUFE: 371 (iv) FEATUFE: 374 (iv) FEATUFE: 375 (iv) FEATUFE: 377 (iv) FEATUFE: 378 (iv) FEATUFE: 379 (iv) FEATUFE: 379 (iv) FEATUFE: 379 (iv) FEATUFE: 379 (iv) FEATUFE: 370 (iv) FEATUFE: 3	60
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W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOPOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA 362 (iii) HYLOTHETICAL: Ma 364 (iv) ANTI-SENSE: Ma 366 (vi) OFIGINAL COUPCE: 376 (iv) FFATURE: 377 (iv) FFATURE: 378 (iv) FEATURE: 379 (iv) FEATURE: 370 (iv) FEATURE: 37	120 180
W> 367 (E) TOPOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA 362 364 (iv) ANTI-SENSE: DE 366 (vi) OFIGINAL COUPTE: 376 377 (iv) FEATURE: 377 (iv) FEATURE: 378 379 (iv) FEATURE: 379 (iv) FEATURE: 370 (iv) FEATURE: 371 (iv) FEATURE: 374 375 (iv) FEATURE: 375 (iv) FEATURE: 376 (iv) FEATURE: 377 (iv) FEATURE: 378 (iv) FEATURE: 379 (iv) FEATURE: 370 (iv) FEAT	120 180 240
W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOPOLOSY: linear W> 360 (ii) MOLECULE TYPE: DNA 362 (iii) HYFOTHECICAL: M. 364 (iv) ANTI-SENSE: IN 366 (vi) OSIGINAL NOUSCE: 306 (iv) FFATURE: 306 (iv) FFATURE: 307 (iv) FFATURE: 308 (iv) FFATURE: 309 (iv) FFATURE: 300 (iv) FFATURE: 300 (iv) FFATURE: 301 (iv) FFATURE: 302 (iv) FFATURE: 303 (iv) FFATURE: 304 (iv) FFATURE: 305 (iv) FFATURE: 307 (iv) FFATURE: 308 (iv) FFATURE: 309 (iv) FFA	120 180
W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOPOLOSY: linear W> 360 (ii) MOLECULE TYPE: DNA 362 (iii) HYLOTHETICAL: No 364 (iv) ANTI-SENSE: No 366 (vi) OFIGNAL DOUBCE: 366 (vi) OFIGNAL DOUBCE: 367 (iv) FRATUPE: 368 (iv) FRATUPE: 369 (iv) FRATUPE: 360 (i	120 180 240 300 360
W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOFCLOSY: linear W> 360 (ii) MOLECULE TYPE: DNA 362 (iii) HYLOTHETICAL: IX 364 (iv) OFIGINAL COURCE: 366 (vi) OFIGINAL COURCE: 367 (iii) FEATURE: 368 (iv) FEATURE: 369 (iv) FEATURE: 360 (iv) FEATURE: 360 (iv) FEATURE: 361 (iv) FEATURE: 362 (iv) FEATURE: 363 (iv) FEATURE: 364 (iv) FEATURE: 365 (iv) FEATURE: 366 (iv) FEATURE: 367 (iv) FEATURE: 368 (iv) FEATURE: 369 (iv) FEATURE: 369 (iv) FEATURE: 369 (iv) FEATURE: 369 (iv) FEATURE: 360 (iv) FEATURE:	120 180 240 300
W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOPOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA (iii) RYLOTRETICAL: IX (iv) ANTI-SENSE: UX (iv) OPE SINAL COUPCE: (iii) FEATURE: (iii	120 180 240 360 360 420 480
W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOPOLOGY: linear W> 360 (ii) MOLECULE TYPE: DNA (iii) RYLOTRETICAL: IX (iv) ANTI-SENSE: UX (iv) OPE SINAL COUPCE: (iii) FEATURE: (iii	120 180 240 300 360 420
W> 367 (C) STRANDEDNESS: HEV - Burma strain (E) TOPOLOSY: linear W> 360 (ii) MOLECULE TYPE: DNA 362 (iii) HYLOTHETICAL: No 364 (iv) ANTI-SENSE: No 366 (vi) OFIGNAL DOUBCE: 366 (vi) OFIGNAL DOUBCE: 367 (iv) FRATUPE: 368 (iv) FRATUPE: 369 (iv) FRATUPE: 360 (i	120 180 240 360 360 420 480





VERIFICATION SUMMARY

PATENT APPLICATION: US/09/851,410

LATE: 6 15 L 1 TIMÁ: 15:56:56

Input Set : N:\Crf3\RULE60\09851410.txt
Output Set: N:\CRF3\06152001\1851410.raw

L:32 M:220 C: Keyword misspelled or invalid format, [A) APPLICATION NUMBER: 1:33 M:32 % C: Keyward misspelled or invalid former, L:50 M:346 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYLE:], SeqNo=1 L:231 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYFE:], SeqNo=3 L:273 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYFE:], SeqNo=4 1:294 M:246 W: Invalid value of Alpha Sequence Header Field, [MØLECYLE TYFE:], Seq!A=5 L:367 M:21: C: Keyword misspelled or invalid : rmat, [37] STRANDEDNESS: L:367 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEENECS:], SeqNo=6 1:36] M:240 W: Invalid value of Alpha Sequence Header Field, [MOLECYLE TYPE:], Seq.W =6 L:1142 M:::10 C: Keyword misspelled or invalid :crmat, [.C) UTRANDEDNESU:] L:1142 M::16 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNEUS:], SeqNc=10 L:1135 M:346 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYFE:], SeqNo=10 L:14:3 M:220 C: Reyword misspelled or invalid :5rmat, (70) STRANDEENESS: L:14(5 M:146 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=11 L:1376 M:..46 W: Invalid value of Alpha Gequence Header Field, (MCLECULE TYFE:), SeqMo=11 L:1477 M:LLO C: Keyword misspelled or invalid format, [(C) STEANDEDNESS:) L:1477 M:.46 W: Invalid value of Alpha Sequence Header Field, [STFANDEDNESS:], SeqNo=12 L:1470 M:246 W: Invalid value of Alpha Sequence Header Field, [MCLECULE TYPE:], SeqNo=12 L:1651 M:130 C: Meyword misspelled or invalid format, {(C) STFANDEDNESS:] L:1651 M:146 W: Invalid value of Alpha Sequence Header Field, [STFANDEDNESS:], SeqNo=17 L:1600 M:220 C: Feyword misspelled or invalid format, ((C) STFANDEDNESS:) L:1680 M:246 W: Invalid value of Alpha Sequence Header Field, [STFANDEDNESS:], SeqNo=18 L:1708 M:230 C: Keyword misspelled or invalid format, ((C) STEANDEDNESS:) L:1708 M:246 W: Invalid value of Alpha Sequence Header Field, [STFANDEENESS:], SeqNc=19 L:1736 M:220 C: Ferword misspelled or invalid format, [(C) STFANDEDNESS:) L:1736 M:246 W: Invalid value of Alpha Sequence Header Field, [STFANDEDNESS:], SeqNo=20